AMENDMENTS TO THE SPECIFICATION

Applicants have previously submitted a corrected sequence listing on October 27, 2008. The amendments below are being made to identify the sequences in the specification with those in the corrected sequence listing. No new matter is believed to be added and entry of these amendments is respectfully requested.

Please replace paragraph [0110] with the following paragraph which has been marked up to show the changes made:

[0110] First, standard curves were generated to determine the efficiency of the PCR with primers for the SULT4A1 splice variant 1 and/or splice variant 2 gene (primers not discriminating between SULT4A1sv1 and SULT4A1sv2):

5'-CAAAGTGGTGGTCAGGAGGGT-3' (~~SEQ ID NO. 3~~ SEQ ID NO:7, nucleotides 2064-2084 of SEQ ID NO:3; ~~SEQ ID NO. 4~~ SEQ ID NO:7, nucleotides 1725-1745 of SEQ ID NO:4) and

5'-CCGTTTCAAATACAGCACCAAG-3' (~~SEQ ID NO. 3~~ SEQ ID NO:8, nucleotides 2110-2131 of SEQ ID NO:3; ~~SEQ ID NO. 4~~ SEQ ID NO:8, nucleotides 1771-1792 of SEQ ID NO:4);

and with specific primers for the SULT4A1 splice variant 1 gene only:

5'-CTGACCCCGATGAGATCG-3' (~~SEQ ID NO. 3~~ SEQ ID NO:9, nucleotides 235-252) and 5'-GGCAGGTGGCTCTTGATGA-3' (~~SEQ ID NO. 3~~ SEQ ID NO:10, nucleotides 340-358);

and with specific primers for the SULT4A1 splice variant 2 gene only:

5'-TCACCTACCCCAAGTCCGT-3' (~~SEQ ID NO. 4~~ SEQ ID NO:11, nucleotides 172-190 of SEQ ID NO:4) and

5'-TTCATACTTGAGAAAAAGCACGT-3' (~~SEQ ID NO. 4~~ SEQ ID NO:12, nucleotides 250-272 of SEQ ID NO:4).

Please replace paragraph [0112] with the following paragraph which has been marked up to show the changes made:

[0112] In an analogous manner, the PCR protocol was applied to determine the PCR efficiency of a set of reference genes which were selected as a reference standard for quantification. In the present invention, the mean value of five such reference genes was determined: (1) cyclophilin B, using the specific primers 5'-ACTGAAGCACTACGGGCCTG-3' (SEQ ID NO: 13) and 5'-AGCCGTTGGTGTCTTTGCC-3' (SEQ ID NO: 14) except for $MgCl_2$ (an additional 1 mM was added instead of 3 mM). Melting curve analysis revealed a single peak at approximately 87 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band of the expected size (62 bp). (2) Ribosomal protein S9 (RPS9), using the specific primers 5'-GGTCAAATTTACCCTGGCCA-3' (SEQ ID NO: 15) and 5'-TCTCATCAAGCGTCAGCAGTTC-3' (SEQ ID NO: 16) (exception: additional 1 mM $MgCl_2$ was added instead of 3 mM). Melting curve analysis revealed a single peak at approximately 85 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (62 bp). (3) beta-actin, using the specific primers 5'-TGGAACGGTGAAGGTGACA-3' (SEQ ID NO: 17) and 5'-GGCAAGGGACTTCCTGTAA-3' (SEQ ID NO: 18). Melting curve analysis revealed a single peak at approximately 87 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (142 bp). (4) GAPDH, using the specific primers 5'-CGTCATGGGTGTGAACCATG-3' (SEQ ID NO: 19) and 5'-GCTAAGCAGTTGGTGGTGCAG-3' (SEQ ID NO: 20). Melting curve analysis revealed a single peak at approximately 83 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (81 bp). (5) Transferrin receptor TRR, using the specific primers 5'-GTCGCTGGTCAGTTCGTGATT-3' (SEQ ID NO: 21) and

5'-AGCAGTTGGCTGTTGTACCTCTC-3' (SEQ ID NO: 22). Melting curve analysis revealed a single peak at approximately 83 °C with no visible primer dimers. Agarose gel analysis of the PCR product showed one single band with the expected size (80 bp).